Poster 11. Use of barley stripe mosaic virus for virus-induced gene silencing and gene expression in various wheat tissues.

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Barley stripe mosaic virus (BSMV)-induced gene silencing (VIGS) has shown to be an effective strategy for rapid functional analysis of genes in the leaf tissues of barley and wheat. To extend the potential of VIGS in wheat, we investigated gene silencing in roots and reproductive tissues, compared severity of VIGS in 12 bread wheat cultivars, and demonstrated the transmission of silencing in three selfed generations of inoculated plants. Out of the 12 bread wheat cultivars, Zak and Eltan were most responsive to the silencing of *phytoene desaturase* (*PDS*), and a range from 53–85% suppression of *PDS* transcripts was observed in various wheat cultivars. Incidence of *PDS* gene silencing ranged from 8–11% in the progeny of pγ.PDSas-inoculated plants, from 53 to 72% in the first selfed generation, and 90–100% in the second selfed generation. Spread of the VIGS vector, monitored using green fluorescent protein, was observed in inoculated leaf tissues, phloem, and root cortex at 10 and 17 days-post-inoculation but was absent in apical meristems and reproductive tissues. An antisense construct of the wheat *coronatine insensitive1* (*TaCOI1*) showed suppression of *TaCOI1* transcripts by 50–70% in the roots and 63–68% in the foliage. Similarly, successful silencing of *seed-specific granule bound starch synthase* (*GBSS*) with antisense and hairpin constructs resulted in up to 81% reduction in amylose content, and silencing of the wheat homologue of disrupted meiosis cDNA1 (*TaDMC1*) resulted in 75–80% suppression of the *TaDMC1* transcripts in pollen mother cells.

Poster 12. Characterizing the lignocellulose pathway in wheat by TILLING Triticum monococcum subsp. monococcum.

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Cellulosic biofuel crops are poised to become a major source of energy in the United States, necessitating the understanding the basic biology underlying the traits that control the utility of wheat biomass as an energy source. Mutagenesis is an important tool in crop improvement and is free of the regulatory restrictions imposed on genetically modified organisms. We are developing 'TILL monococcum' a resource for discovery of chemically induced mutants in the diploid wheat ancestor (*T. monococcum* subsp. *monococcum*) to better understand basic wheat biology. A TILLING population of 2,700 single M_2s was developed in *T. monococcum* subsp. *monococcum* using EMS mutagenesis (0.24% EMS). Pools of four M_2 plants were used to screen for lignocellulose pathway mutants in the TILLING population using Cel-I endonuclease. In our preliminary experiments with RT- PCR, 16 ESTs (homologous with annotated genes for lignin precursors in rice) showed a significant developmental regulatory pattern and were in close agreement with total lignin content. Primers were designed from all 16 ESTs for screening the TILLING population. One mutant each was identified for the *PAL 6* and *HCT* locus from the first 716 M_2s screened. The genomic constitution of the selected mutants was determined by Cel-I digestion of the M_3 progeny. Phenotypic validation for the total lignin content of the mutants will be done at maturity.